30 D
Population and Community Dynamics

Populations are the functioning units of individual species. Individuals within a population vary due to their genetic diversity and the demands of their environment, and interact with each other in many ways. Many populations together make up an ecological community, in which each population interacts with the others. These interactions, rather than the individuals or species themselves, provide both stability and the potential for dynamic change in the ecosystem. In many ecosystems, such as in the boreal forest shown here, the biotic and abiotic components of the environment vary with the seasons. Population ecologists document and interpret the interactions, quantifying the changes that occur over time.

In this unit, you will gain an understanding of the variety of interactions both within populations and among the populations in a community. You will use this understanding to examine the very successful growth of our own species and our changing relationships with the other organisms on Earth.

As you progress through the unit, think about these focusing questions:

• How does one determine if populations are changing over time?

• In what ways may individual members of a population interact with one another or with members of a different population?

• What quantitative measures indicate that populations change over time?

UNIT 30 D PERFORMANCE TASK
Changes in Human Population Size

The United Nations estimates that the global human population is greater than 6 billion people. About 100 000 years ago, only a few thousand people lived on Earth. What factors contributed to this growth? How did humans become such a successful species? At the end of this unit, you may apply your skills and knowledge to complete this Performance Task.

GENERAL OUTCOMES

In this unit, you will

- describe a community as a composite of populations in which individuals contribute to a gene pool that can change over time
- explain the interaction of individuals in populations with each other and with members of other populations, the basis of which is genetic variation
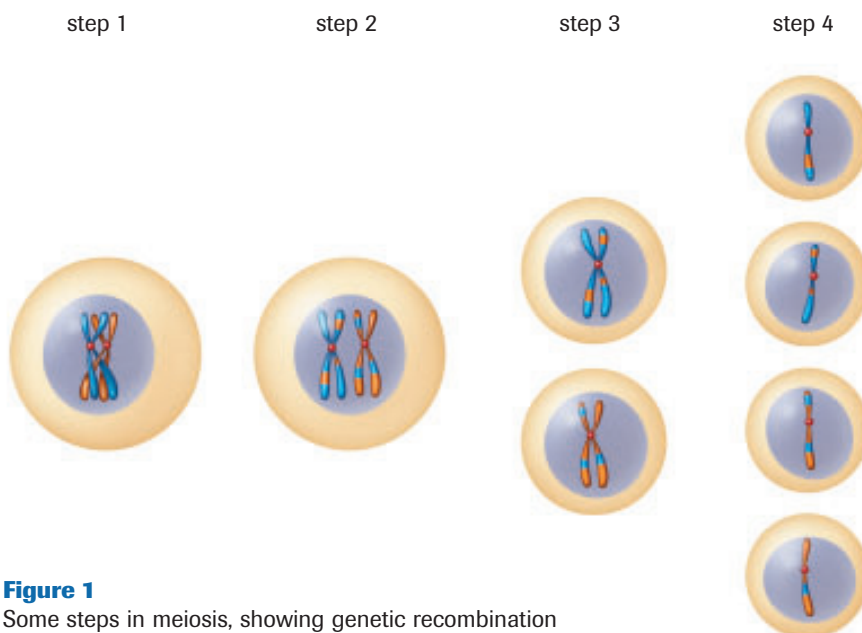- explain, in quantitative terms, the changes in populations over time

ARE YOU READY?

These questions will help you find out what you already know, and what you need to review, before you continue with this unit.

Knowledge

1. In your notebook, indicate whether the statement is true or false. Rewrite a false statement to make it true.
   (a) Mutations are changes in DNA that are harmful to the cell.
   (b) Sexual reproduction is disadvantageous because the offspring show little or no genetic diversity.
   (c) Through the process of genetic recombination, meiosis produces diploid cells and increases the potential diversity of offspring.
   (d) In species that reproduce asexually, offspring are always genetically identical to their parent.
   (e) Over time, dominant alleles will tend to become more common in a population, while recessive alleles will become more rare.
   (f) An organism's genotype refers to its genetic makeup, which is unaffected by the environment.
   (g) An organism's phenotype refers to traits that are expressed in the organism and affected by both its genotype and the environment.
   (h) A species is a population or populations of organisms that are able to interbreed under natural conditions and produce fertile offspring.
   (i) Harmful or lethal mutations have little or no effect on the health of large multicellular organisms.
   (j) Virtually all large populations exhibit genetic variation among individuals.

2. Define these terms:
   (a) exotic species   (d) food web
   (b) carrying capacity   (e) biotic factors
   (c) food chain   (f) abiotic factors

3. **Figure 1** shows four steps in meiosis that contribute to genetic recombination. Explain what event is occurring in each step, and how each step contributes to increased genetic variation of gametes.

step 1   step 2   step 3   step 4

Figure 1
Some steps in meiosis, showing genetic recombination

Skills

4. Examine the Punnett square in **Figure 2**, which represents a cross between a male that is homozygous for two dominant alleles, *AA* and *HH*, and a female that is homozygous for two recessive alleles, *aa* and *hh*.
   (a) Have the variety and ratio of genotypes changed in the F_1 generation?
   (b) In the parent generation, state the ratio of the specific alleles for each gene (i.e., *A:a* and *H:h*).
   (c) Taking all F_1 individuals into consideration, do the allele ratios change in the F_1 generation? Explain your reasoning.
   (d) Draw a Punnett square and determine the allele ratios for the F_2 generation.

gametes ➤	*ah*	*ah*
AH	*AaHh*	*AaHh*
AH	*AaHh*	*AaHh*

Figure 2
Punnett square analysis of a dihybid cross

5. Zebra mussels often grow in high concentrations on water intake pipes. Assume that **Table 1** represents the number of mussels per square metre of pipe surface sampled over a 10-year period.
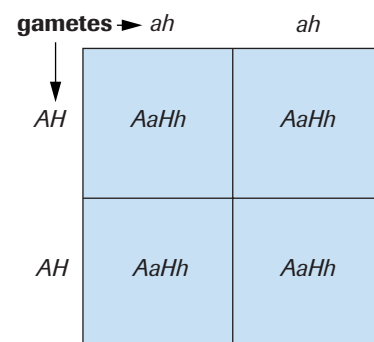
Table 1 Zebra Mussel Population in a Small Water Body, 1991–2000

Year	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000
Population (per m²)	400	520	676	879	1142	1485	1930	2509	3262	4241

   (a) Draw a population curve for the zebra mussel population from 1991 to 2000. Label your axes, and give your graph an appropriate title.
   (b) Describe the growth illustrated by your graph.
   (c) Calculate the population growth rate of zebra mussels from 1996 to 2000.
   (d) If no measures are taken to control the zebra mussel population in this location, hypothesize what the population would be in 2010. Add these data to your graph.
   (e) What factors are likely to limit the growth of this zebra mussel population?

STS Connections

6. For each of the following, list two examples, one that is not genetically inherited and one that might have been genetically inherited:
   (a) physical characteristics
   (b) diseases and medical conditions
   (c) behaviours, and likes and dislikes

7. Zebra mussels clog pipelines and other underwater structures (**Figure 3**). What economic and other social impacts could this problem cause?

8. In January 2002, the North American Commission for Environmental Cooperation released a report that declared that North America is facing a "widespread crisis" because of its shrinking biodiversity.
   (a) How is the loss of biodiversity related to the loss of genetic diversity?
   (b) Why do so many scientists, government agencies, and members of the public consider it an important issue?

Figure 3
Zebra mussels

The Genetic Basis for Population Change

We have all noticed that certain traits are inherited from generation to generation (**Figure 1**). In *On the Origin of Species,* Charles Darwin provided compelling evidence for evolution and natural selection. About 70 years after Darwin's work, scientists finally understood how parents' traits are inherited by offspring. Now, geneticists can distinguish the genetic code of one individual from those of a whole population. This powerful science is also being used to measure the genetic differences between entire species and to document changes in the genetic makeup of populations over surprisingly short periods of time.

💡 STARTING Points

Answer these questions as best you can with your current knowledge. Then, using the concepts and skills you have learned, you will revise your answers at the end of the chapter.

1. Successful individuals of a species are able to reproduce and adapt to their environments. What role might their genetic makeup play in meeting these two demands?

2. The population size of marine green sea turtles (**Figure 2 (a)**) shows little change over time while the locust population in the Canadian prairies (**Figure 2 (b)**) varies widely from year to year. What might this suggest about the environments in which they live? Which environment is the most stable?

(a)   **(b)**
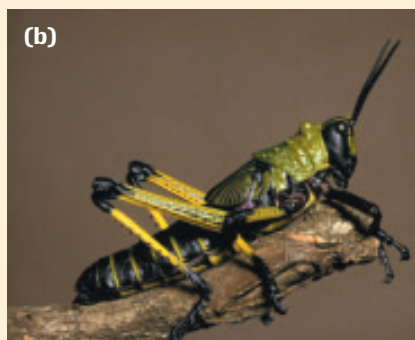
Figure 2
(a) green sea turtle
(b) locust

Career Connections:
University Professor; Anthropologist

Figure 1
Although individuals in a population have some unique traits, other traits are common to all the members.

▶ *Exploration*   *Distinguishing Traits*

Study the photo of the group of people in **Figure 1**. These individuals exhibit variations, but they also share such inherited physical features as limbs, internal organs, and paired eyes and ears. Yet pigeons, alligators, horses, and toads also possess these features.

(a) List inheritable features by which you can distinguish human beings from all other species.

(b) List inheritable features by which you can distinguish human individuals from one another.

(c) On each list, circle the two or three most significant distinguishing traits.

(d) Are the most distinguishing traits from parts (a) and (b) unique to each species and individual respectively, or do they represent variations of shared features?

The Genetic Basis for Population Change

Figure 1
The genetic diversity of many populations, such as this one of long-nosed bats, may not be readily apparent.

Recall from Unit 30 C that all individuals of the same species possess a common genome, except for sex chromosomes (when present). However, each individual has a different genotype. Differences in genotypes and environmental influences account for differences among the phenotypes of individuals of the same species. These different phenotypes are then acted on by natural selection.

Traits that distinguish individuals from one another represent genetic diversity, which varies both within species and from species to species (**Figure 1**).

With techniques such as DNA sequencing, geneticists have begun to analyze and compare the genetic code of individuals, populations, and entire species. One finding is that the amount of DNA present in different species varies dramatically, as shown by the examples in **Table 1**. Organisms with larger genomes have the potential for greater genetic diversity and present more targets for mutation.

The size of genomes, however, does not provide an accurate comparison of a species' genetic diversity. Genomes of many eukaryotic organisms, for example, contain DNA that is not transcribed. Some noncoding sequences in the genome of humans, as well as other organisms, may be repeated as many as 500 000 times. Some species, such as maize or wheat, are polyploids. This means that the species has more than two copies of each chromosome, resulting in multiple, often identical, copies of the same genes.

Regardless of the total quantity of DNA present, most species (other than some microorganisms) have large numbers of different genes—usually numbering in the thousands. Species that possess a larger number of genes have the potential for increased genetic diversity. Similarly, the greater the number of different alleles for these genes, the more genetic variation there will be between individuals in a species. For species that undergo sexual reproduction, genetic diversity within a population increases enormously when the various alleles from two parents recombine at fertilization.

As you learned in Chapter 6, all of the genes that occur in a population are referred to as the gene pool. The gene pool maintains continuity of traits from generation to generation. Although some gene frequencies remain the same over many generations, others change quickly.

Table 1 Total Amount of DNA in the Genomes of Selected Species

Species	Common name	DNA (kilobases)
Mycoplasma genetalium	bacterium	580
Saccharomyces cerevisiae	yeast	1200
Drosophila melanogaster	fruit fly	180 000
Xenopus laevis	toad	3 100 000
Macaca nigra	macaque	3 399 900
Homo sapiens	human	3 400 000
Necturus maculosus	mud puppy	81 300 000
Amphiuma means	newt	84 000 000
Trillium species	trillium	100 000 000
Amoeba dubia	amoeba	670 000 000

Case Study—Global Variation in Blood Type

Blood type is an inherited characteristic. Each individual has type A, B, AB, or O blood, and also either Rh negative (Rh−) or Rh positive (Rh+). The alleles responsible for these blood types are designated as I^A, I^B, I^O, $Rh+$, and $Rh−$.

Your ABO blood type was determined by the direct inheritance of one allele from each of your parents; it cannot be altered by any environmental factor. As a result, blood types are ideally suited for the study of human genetic variation and provide dramatic evidence of human genetic diversity at the population level.

In this activity, you will examine the geographic distribution of different blood types in humans. You will analyze these patterns and relate them to human genetic diversity, and use your understanding of genetics and populations to account for the distribution patterns.

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▶ **EXPLORE** an issue

Are Human "Races" Only Skin Deep?

Issue Checklist

○ Issue	● Design	● Analysis
● Resolution	● Evidence	● Evaluation

The geographic distribution patterns of blood alleles is not the same as the distribution patterns of skin colour and "race." This means that skin colours and blood types do not evolve in the same way. Thus, the whole notion of categorizing humans into "races" may be in error. Research the following and discuss your answers in a small group.

(a) How do we identify human "races"?

(b) What human skin colours are associated with what major landmasses?

(c) What environmental factor(s) are most likely responsible for the distribution of alleles that influence skin colour?

(d) A scientist proposes that governments define an individual's "race" according to his or her "blood type." The scientist argues that blood type is a much better indicator of human "relatedness" than skin colour.

   (i) Is the scientist's argument valid? Is blood type more biologically significant than skin colour?

   (ii) Is the concept of human "race" scientifically valid at all? Is it reasonable to group people according to a small genetic difference simply because it is visible?

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Hardy–Weinberg Principle and Population Equilibrium

Population geneticists have developed a method to quantify a gene pool—the genetic information of an entire population—by measuring each **allele frequency**. Thus, changes in populations can be measured in part by looking for changes in allele frequencies. Note that not all genes exhibit variation. Where only a single allele exists for a particular gene, that allele's frequency is 100 % and it is described as a **fixed frequency**.

Consider a population of moths for which there are two alleles, *A* and *a*, where *A* represents the allele for dark brown wings, which is dominant, and *a* represents the allele for light brown wings, which is recessive. A population of 500 comprises 320 moths with *AA* homozygous dark wings, 160 moths with *Aa* heterozygous dark wings, and 20 moths with *aa* homozygous light brown wings. Each individual contributes two alleles to the gene pool, giving 640 *A* (from *AA* genotype), 160 *A* + 160 *a* (from *Aa* genotype), and 40 *a* (from *aa* genotype).

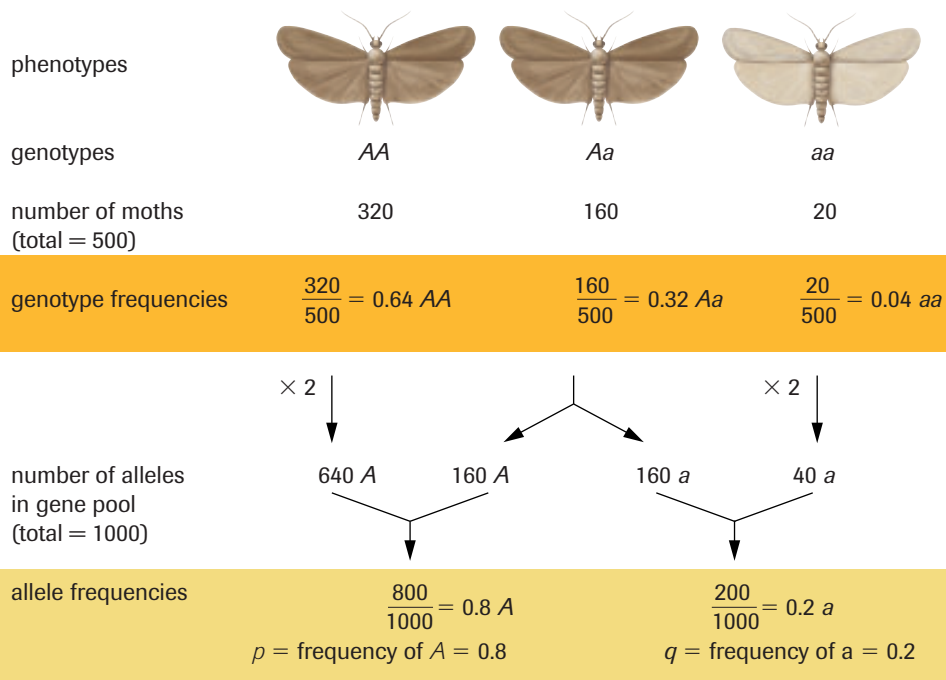**allele frequency** the proportion of gene copies in a population of a given allele

fixed frequency the frequency of an allele within a population when only a single allele is present for a particular gene (i.e., the allele's frequency is 100 %)

phenotypes			
genotypes	*AA*	*Aa*	*aa*
number of moths (total = 500)	320	160	20
genotype frequencies	$\frac{320}{500} = 0.64$ *AA*	$\frac{160}{500} = 0.32$ *Aa*	$\frac{20}{500} = 0.04$ *aa*

× 2   × 2

number of alleles in gene pool (total = 1000)	640 *A* 160 *A*	160 *a* 40 *a*	
allele frequencies	$\frac{800}{1000} = 0.8$ *A*	$\frac{200}{1000} = 0.2$ *a*	
	p = frequency of *A* = 0.8	q = frequency of a = 0.2	

Figure 2
The allele frequencies of a population of moths

The allele frequency for *A* is 800 ÷ 1000 = 0.80, or 80 %, and that of *a* is 200 ÷ 1000 = 0.20, or 20 % (**Figure 2**). Would the dominant form of moth wing become more and more common over time? Do allele frequencies remain constant or change over time?

These questions interested Reginald Punnett. Over a meal in 1908, Punnett posed them to Godfrey Hardy, an eminent mathematician, who, without hesitation, wrote a solution on a napkin. Working independently, German physician Wilhelm Weinberg formulated the same solution. Now referred to as the Hardy–Weinberg Principle, this mathematical relationship, outlined below, shows that allele frequencies will not change from generation to generation, as long as certain conditions are met.

Conditions of the Hardy–Weinberg Principle

Allele frequencies in a population will not change if

- the population is infinitely large
- no migration occurs
- no mutations occur
- no natural selection occurs
- mating is random

For a gene with only two alleles (*A* and *a*), the Hardy–Weinberg Principle can be expressed using the following equation:

If p = frequency of allele *A* and q = frequency of allele *a*, then

$$p + q = 1$$
$$(p + q)^2 = 1^2$$

and so $\quad p^2 + 2pq + q^2 = 1$

p^2 = frequency of genotype *AA*
$2pq$ = frequency of genotype *Aa*
q^2 = frequency of genotype *aa*

This equation gives the expected genotype frequencies of the population, when all the conditions of the Hardy–Weinberg Principle are met. We will refer to it as the Hardy–Weinberg equation. Note that after a single generation of random mating, the genotype frequencies are given by p^2, $2pq$, and q^2.

Applying the Hardy–Weinberg Principle

For the moth population in **Figure 2**, on the previous page, the allele frequency of the *A* allele is 0.80, or 80 %, and the frequency of the *a* allele is 0.20, or 20 %. If mating is random, when the population reproduces, 80 % of all gametes will bear the *A* allele, while the remaining 20 % of gametes will bear the *a* allele. The genetic recombination that occurs in the next generation is shown in **Figure 3**. Substituting these values into the Hardy–Weinberg equation, we get the following:

$$(0.80)^2 + 2(0.80)(0.20) + (0.20)^2 = 1$$
$$0.64 + 0.32 + 0.04 = 1$$

Therefore, the frequency of the *AA* genotype is 0.64, or 64 %, the frequency of the *Aa* genotype is 0.32, or 32 %, and the frequency of the *aa* genotype is 0.04, or 4 %. The genotype frequency values of offspring generations are the same as those for the parent generation. If random mating continues to occur, allele frequencies are likely to remain constant from generation to generation.

Genetic structure of second generation

Recombination of alleles from first generation (parents)
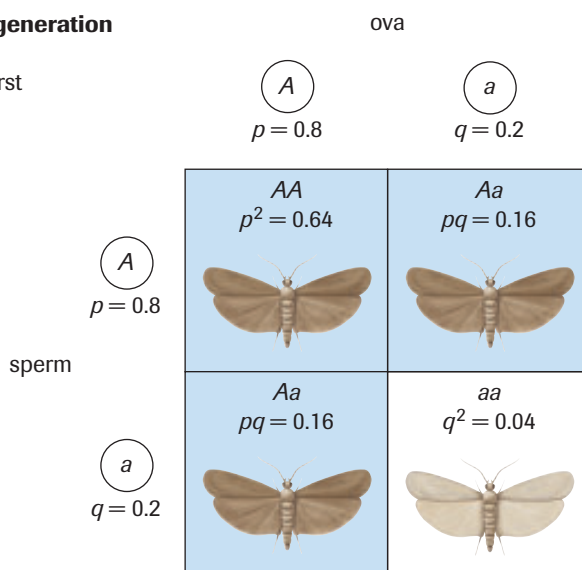
Figure 3
A typical Punnett square shows a cross between two individuals. This one depicts the allele frequencies of offspring within the moth population in **Figure 2** on the previous page.

Apply the Hardy–Weinberg equation to solve the following problem, assuming that all five of the Hardy–Weinberg conditions are met:

A population has only two alleles, *R* and *r*, for a particular gene. The allele frequency of *R* is 20 %. What are the frequencies of *RR*, *Rr*, and *rr* in the population?

Solution

If *p* represents the frequency of allele *R*, *q* the frequency of allele *r*, and *p* = 0.20, then *q* = 0.80. Using the equation for the Hardy–Weinberg Principle, we get the following:

$$(0.20)^2 + 2(0.20)(0.80) + (0.80)^2 = 1$$
$$0.04 + 0.32 + 0.64 = 1$$

frequency of *RR* genotype = 0.04, or 4 %

frequency of *Rr* genotype = 0.32, or 32 %

frequency of *rr* genotype = 0.64, or 64 %

Learning Tip

Turn to Appendix A7, Math Skills, for a review of how to correctly perform calculations using scientific notation.

▶ **Practice**

For all questions, assume that the conditions for the Hardy–Weinberg Principle are being met.

1. A large population consists of 400 individuals, of which 289 are homozygous dominant (*MM*), 102 are heterozygous (*Mm*), and 9 are homozygous recessive (*mm*). Determine the allele frequencies of *M* and *m*.

2. The gene pool of a certain large population of fruit flies contains only two eye-colour alleles: the dominant red allele, *R*, and the recessive white allele, *r*. Only 1 % of the population has red eyes. Determine the allele and genotype frequencies of this population.

3. Manx cats have no tails (or have very short tails) and have large hind legs. The no-tail trait results from a heterozygous genotype, *Tt*. Interestingly, *TT* genotypes are normal cats, while the *tt* genotype is lethal and cat embryos that possess it do not survive. In a population of 1000 cats, only 1 % are Manx and 99 % are normal.
   (a) What are the allele frequencies in this population?
   (b) Determine the expected frequency of each genotype in the next generation.
   (c) Determine the allele frequencies of the population of cats from (b).
   (d) What influence do homozygous recessive genotypes have on allele frequencies in this generation?
   (e) Predict the long-term result of a lethal homozygous recessive trait in a wild population.

🖑 W W W **WEB** *Activity*

Simulation—Hardy–Weinberg

In this activity, you will visit links on the Nelson Web site to observe various simulation models of populations. These simulations allow you to manipulate the conditions necessary for maintaining Hardy–Weinberg equilibrium. Your tasks are to

- experimentally test the effect of altering each condition
- critique at least two different simulation models and assess their strengths and weaknesses

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Quantifying Human Genetic Variation

Humans possess several easily distinguishable traits, each of which is controlled by a single recessive and dominant allele combination.

- Select two of the following traits:
  – blue eyes
  – widow's peak
  – hitchhiker's thumb
  – attached earlobes
  – freckles
  – dimples
  – tongue rolling
  – long second toe (second toe extends beyond big toe)
- Research to determine if the trait is controlled by a dominant or a recessive allele.
- Survey at least 20 students in your class and record the presence or absence of the trait. If possible, share data with other classes to increase the sample size.

- Apply your understanding of genetics and the Hardy–Weinberg equation to estimate population allele frequencies.
- Conduct research to find the accepted allele frequency values.

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(a) How would your data have differed if you had surveyed your family members instead of students?
(b) Suggest methods you could use to determine if the alleles you studied were in Hardy–Weinberg equilibrium.
(c) Account for any differences between your findings and the accepted allele frequency values for the human population.

SUMMARY   *The Hardy–Weinberg Principle*

- The gene pool of a population is determined by the alleles possessed by the individuals in the population. A gene pool can be quantified by measuring the allele frequency.
- According to the Hardy–Weinberg Principle, the gene pool of a population will not change when the following conditions are met:
  – The population is infinitely large.
  – No migration occurs.
  – No mutations occur.
  – No natural selection occurs.
  – Mating is random.
- When the Hardy–Weinberg conditions are met, then, for a gene with two alleles (A and a), the allele frequency in the population will be

$$p + q = 1$$

  where $p = $ frequency of allele A and $q = $ frequency of allele a
- When all the Hardy–Weinberg conditions are met, then, for a gene with two alleles (A and a), the genotype frequency in the population will be

$$p^2 + 2pq + q^2 = 1$$

  where $p^2 = $ frequency of genotype AA, $2pq = $ frequency of genotype Aa, and $q^2 = $ frequency of genotype aa

1. Describe how the genetic diversity of a population is influenced by recombination and heterozygosity.

2. Study **Table 1** on page 716.
   (a) Suggest possible reasons that might account for the widely varying amounts of DNA found in these species.
   (b) *Necturus* and *Amphiuma* have similar sized genomes. Why is this not surprising?
   (c) The size of the genome does not provide any information on the genetic variability within chromosomes. How might polyploidy, non-coding sequences, and multiple alleles contribute to the genetic diversity of species?

3. Describe how gene duplication and recombination during meiosis contribute to the overall genetic diversity of populations.

4. Use the Punnett square in **Figure 4** to briefly explain how sexual reproduction increases the potential for genetic variation.

♂parent
RrTt

	RT	Rt	rT	rt
RT	RRTT	RRTt	RrTT	RrTt
Rt	RRTt	RRtt	RrTt	Rrtt
rT	RrTT	RrTt	rrTT	rrTt
rt	RrTt	Rrtt	rrTt	rrtt

♀ parent
RrTt

Figure 4
A Punnett square showing the offspring of parents with identical genotypes and phenotypes. The possible phenotypes are represented in different-coloured cells.

5. For each of the following, predict whether Hardy–Weinberg equilibrium would be maintained generation after generation:
   (a) a population of African violets maintained by a plant breeder
   (b) the population of mosquitoes in northern Alberta
   (c) an elk population living in Banff
   (d) a newly discovered bird population on a remote island off the coast of British Columbia

6. A population of 200 includes 32 individuals that are homozygous recessive (*bb*) for a given trait. Assuming the population meets the conditions for Hardy–Weinberg equilibrium, how many of the 200 individuals would you expect to be homozygous dominant (*BB*)?

7. Cystic fibrosis is a recessive condition that affects about 1 in 2500 people in the Caucasian population of Canada. Calculate the following:
   (a) the population frequencies for the dominant (*C*) and recessive (*c*) alleles
   (b) the percentage of the population that is a carrier of the recessive allele
   (c) the number of students in your school that are likely to be carriers of the cystic fibrosis allele

8. A recessive allele (*h*) codes for complete hair loss in chimpanzees. Homozygous recessive individuals lose all their hair by about six months of age. Chimpanzees with one or two dominant alleles (*H*) show no signs of this disorder. In a population of captive chimpanzees, 16 % of the chimpanzees lose all their hair.
   (a) Calculate the allele frequencies of *H* and *h*.
   (b) What percentage of the chimpanzees could *not* be the parents of chimpanzees with this condition.
   (c) Hairless chimpanzees have reduced survival rates and lower reproductive success. Predict how the allele frequencies will change over time. Explain your reasoning as it relates to the Hardy–Weinberg equilibrium assumptions.

The Hardy–Weinberg Principle predicts that, under a set of specific conditions, a gene pool will remain unchanged from generation to generation. The underlying conditions are critically important. When the conditions of the Hardy–Weinberg Principle are not met, a gene pool is predicted to change in the following ways:

- When a population is small, chance fluctuations will cause changes in allele frequencies.
- When individuals migrate, they will remove alleles from one population and add them to another.
- When mutations occur, new alleles will arise or one allele will be changed into another, thereby changing the allele frequencies in the population.
- When natural selection occurs, individuals with certain alleles will have greater reproductive success than others do, thereby increasing the relative frequency of their alleles in the next generation.
- When mating is not random, individuals that are preferred as mates will pass on their alleles in greater numbers than less preferred mates.

Real populations can be affected by any of these conditions, resulting in changes to allele frequencies in the gene pool.
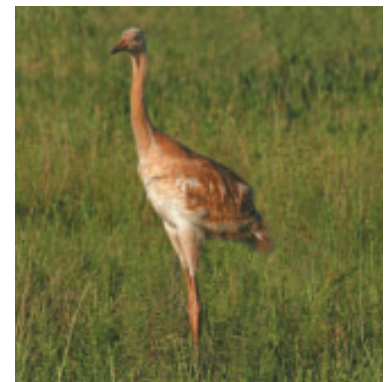
Genetic Drift

Genetic drift is a change in the genetic makeup of a population resulting from chance. When populations are small, chance can significantly alter allele frequencies. For example, assume that only 1 in 100 whooping cranes carries a particular allele, C_1 (**Figure 1**). If the whooping crane population had 10 000 individuals, you would expect 100 birds to carry the allele. If half the population died in a severe storm, for example, about 50 of the 5000 survivors would have the C_1 allele. Therefore, the allele frequency is not expected to change significantly. If the whooping crane population is only 200 individuals, only two birds would have the C_1 allele. If half of this population died, both the C_1 carriers could die, eliminating the C_1 allele entirely. If both survived, then the C_1 allele frequency would double.

Figure 2, on the next page, shows how population size affects genetic drift. **Figure 2 (a)** illustrates genetic drift in a population of 25 stoneflies. The frequency of allele *A* fluctuates wildly from generation to generation. In five of the trials, the *A* allele frequency became fixed at 100 % in 22 generations or fewer. In the other four trials, the *A* allele was lost entirely in 36 generations or fewer. In a larger population of 500 stoneflies, shown in **Figure 2 (b)**, the allele frequency remained relatively stable even after 50 generations had passed. There was no trend toward fixing of the allele. In small populations, genetic drift can lead to fixation of alleles. This increases the percentage of homozygous individuals within a population and reduces its genetic diversity.

When a few individuals from a large population leave to establish a new population, the resulting genetic drift is called a **founder effect**. The allele frequencies of the new population will likely not be the same as those of the original population and may deviate further as the new population expands. Founder effects seem to be common in nature, such as when a few seeds carried by a bird or by winds to a distant volcanic island may germinate and rapidly establish a large population. With self-pollinating plants, an entire population can be established from a single fertile seed. Founder effects can also be seen in

genetic drift changes to allele frequency as a result of chance
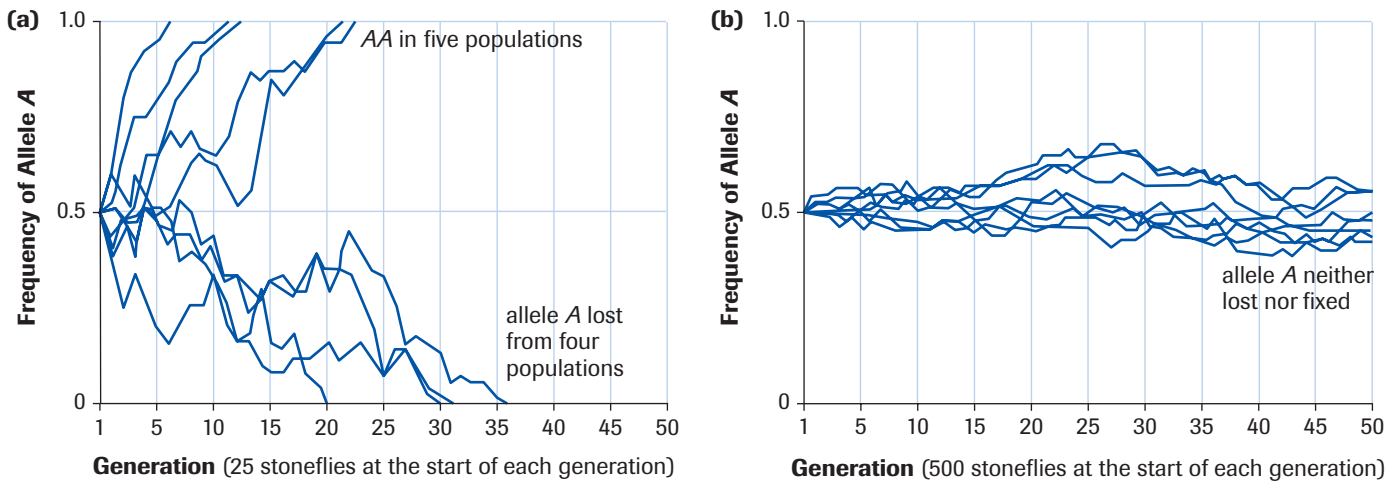

Figure 1
A young whooping crane. In 1941, there were only 22 individuals left in Alberta. Today, the breeding population in Wood Buffalo National Park remains very susceptible to the effects of genetic drift.

founder effect genetic drift that results when a small number of individuals separate from their original population and find a new population

(a) *AA* in five populations

allele *A* lost from four populations

Generation (25 stoneflies at the start of each generation)

(b) allele *A* neither lost nor fixed

**Generation** (500 stoneflies at the start of each generation)

Figure 2
(a) In small populations, genetic drift can result in dramatic changes in allele frequencies.
(b) In larger populations, genetic drift is not usually significant.

human populations. Members of the Amish community in Pennsylvania are all descendants of about 30 people who emigrated from Switzerland in 1720. One of the founders had a rare recessive allele that causes unusually short limbs. The frequency of this allele in the current Amish population is about 7 %, compared to a frequency of 0.1 % in most populations.

When a severe environmental event results in a drastic reduction in population size, a population may experience a **bottleneck effect** (**Figure 3**). With the bottleneck effect, the frequency of alleles in the survivors is very different from that in the original population. Additional genetic drift may result in further changes in the gene pool. This is known to have occurred with the northern elephant seal (**Figure 4**).

bottleneck effect a dramatic, often temporary, reduction in population size, usually resulting in significant genetic drift

parent population   bottleneck (drastic reduction in population)   surviving individuals   next generation
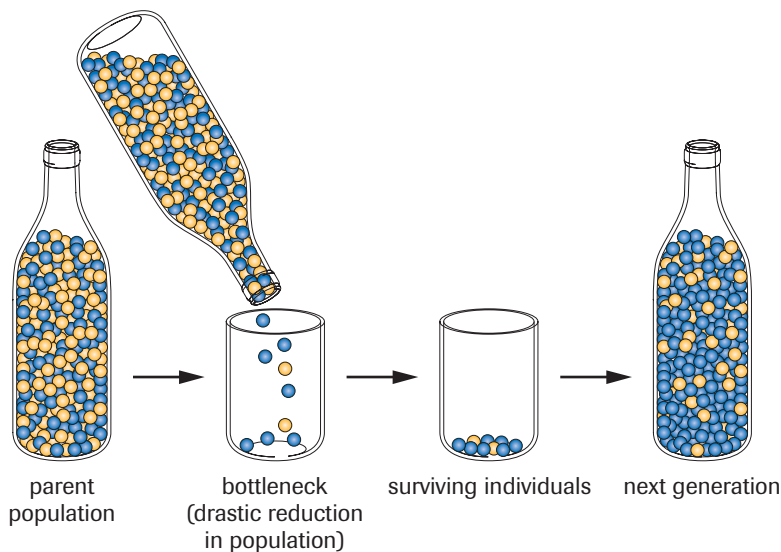
Figure 3
A dramatic, sometimes temporary, reduction in the size of a population can result in a bottleneck effect.

Figure 4
The northern elephant seal population was reduced by overhunting to 20 individuals in the 1890s. Although the population had rebounded to over 30 000 individuals by 1974, 24 gene loci were found to be homozygous by genetic testing.

> ▶ mini *Investigation*   *Demonstrating Chance*
>
> See for yourself how random chance works in small populations.
>
> A large population of birds possesses six different alleles for a specific gene. All alleles are present in equal frequencies. Assume that 30 individuals are randomly separated from the original population and become established on a remote island. Let the alleles be represented by the numbers 1 to 6.
>
> - Model the initial allele frequency of the new population by tossing a six-sided die 30 times. Record your results.
> - Examine the results obtained by your classmates.
>
> (a) How often did you roll a three? Did your response differ from the one-sixth you would expect by chance?
>
> (b) How many times did you roll a three in your first six tosses? What ratio did this produce?
>
> (c) Relate the variations in the frequencies of the number three to variations in allele frequencies that occur when small founder populations form.

Gene Flow

When organisms migrate, leaving one population and joining another, they alter the allele frequencies of both populations. Such **gene flow** occurs frequently in most wild populations. For example, prairie dogs live in dense colonies consisting of a few dozen members. For much of the year they prevent other prairie dogs from joining their colony. In late summer, however, mature male pups are permitted to enter new colonies, thereby affecting both gene pools. New alleles may be added or rare alleles lost during such events. Gene flow can also occur when individuals of adjacent populations mate without moving permanently. In these ways, genetic information is shared between populations. Unlike genetic drift, gene flow tends to reduce differences between populations.

gene flow the movement of alleles from one population to another through the movement of individuals or gametes

Mutations

As you have previously learned, mutations are randomly occurring events that alter the inheritable genetic material of an individual. Mutations are the source of new genetic diversity in a species as a whole. Mutations vary considerably in size. They range from the alteration of a single base pair in a DNA molecule to large-scale changes such as multi-base-pair deletions, insertions, or inversions.

Many mutations are neutral mutations, and have no effect on the individual or its reproductive success. Other mutations may be beneficial mutations (enhancing reproductive success) or harmful mutations (reducing reproductive success). You will find more information about mutations in Chapters 5 and 20. When a mutation arises in a population, it has the potential to alter the gene pool or allele frequencies of the population, and therefore the Hardy–Weinberg equilibrium. However, the mutation will not influence the entire population or species unless the resulting genetic change becomes relatively common. Genetic changes resulting from mutations become common when they are beneficial to the individuals that possess them. As you have learned, inheritable characteristics that are favoured by natural selection become more common over time. Since these traits are determined by specific alleles then, as a result of natural selection, the allele frequencies (or genetic makeup) of a population will change over time. Most natural populations are large and reproduce rapidly, with each new individual inheriting a very large number of alleles. Although the chances of a mutation arising in any specific allele are low, new mutations arise often and continuously in the population as a whole.

DID YOU KNOW ❓

Lots of Mutations

It has been estimated that each new human cell contains about 100 new mutations. Although this number seems high, most of the mutations occur in non-coding DNA sequences.

The Genetic Basis for Population Change **725**

Genetic Diversity at Risk

In this activity, you will examine several significant threats to genetic diversity that face both wild and domesticated species, and learn how biologists and conservationists are addressing these threats. What do you already know about the Threats listed in **Table 1**? Are you familiar with any of the Actions that are being taken to preserve genetic diversity?

- Share your prior knowledge about these topics with members of your group.
- Choose one Threat and a related Action with your group. For example, you might choose the loss of crop-seed varieties (Threat) and the establishment of seed banks (Action).
- Conduct some preliminary research to determine the general nature of the Threat and the Action. During your research, document the global status of the Threat and the scope of the Action. Consider the factors that are driving the Action. What are the underlying causes of this Threat and what are the motivating concerns behind the Action? Consider both the short-term and long-term implications of

the Threat and the Action. What is predicted to happen if the current Threat persists or if the Action is unsuccessful?

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- When research is completed, select examples you think best exemplify the Threat and Action you reviewed. Conduct more in-depth research on these examples and document your findings.

(a) Prepare a class presentation on your Threat and Action. Make sure that your presentation
 – provides an overview of the Threat and the Action
 – accounts for the root cause of the Threat
 – highlights examples in detail
 – relates the topic directly to the impact of human activities
 – includes a summary flowchart that relates the Threat to the Action

Table 1 Some Threats to Genetic Diversity and Actions to Reduce Its Effect

| Threats to genetic diversity	Actions to protect genetic diversity
• habitat loss such as clearing of tropical rainforests, elimination of wild-grass prairies, and coral-reef bleaching • over-harvesting of individual species • fragmentation of wilderness, leading to small isolated populations • competition with exotic species • loss of traditional domesticated animal and plant crop varieties	• establishment of natural reserves and parks • international treaties to protect species and ecosystems • direct protection of endangered species and their primary habitat • creation of gene and seed "banks" • captive animal- and plant-breeding programs in zoos and botanical gardens

Selection of Another Hemoglobin Allele?
In November 2001, geneticists reported in the journal *Nature* about another mutated form of the hemoglobin gene that provides resistance to malaria. Unlike the sickle-cell allele (*HbS*), individuals with two copies of the *HbC* allele show no signs of disease and are very resistant to even the most serious form of malaria. Interestingly, the mutation in the β-hemoglobin gene that produced the *HbC* allele is in the identical location as the *HbS* allele.

Natural Selection

Mutations provide a continuous supply of new genetic variations, which may be inherited and expressed as different phenotypes. Natural selection then acts on these mutations. Although mutations provide the source of variation, natural selection acts on individuals and their phenotypes. As a result, particular alleles are most successful and passed on when they enhance the phenotype of the individual and, thereby, contribute to their reproductive success. Selective forces can favour particular variations in the phenotype of individuals in a number of ways. Sickle-cell anemia, a potentially serious blood disorder, is a useful example of how mutation, genetic variation, and the environment result in different patterns of natural selection.

The allele for sickle-cell anemia differs from the normal hemoglobin gene by a single base-pair mutation. Individuals homozygous for the sickle-cell allele are severely afflicted with this disorder. Heterozygous individuals are only mildly affected by sickle-cell anemia; however, they are much more resistant to malaria than are people with normal hemoglobin. In regions where malaria is uncommon, individuals with the sickle-cell allele are at a disadvantage and their phenotypes are less likely to contribute alleles to the gene pool. But in regions where malaria is common (**Figure 5**), heterozygous individuals are strongly favoured; they are much more likely to survive and pass on their genes to the next generation. The environment selects the best-adapted phenotype and, in so doing, favours a particular set of alleles.

(a)

**P. falciparum
malaria in Africa**

☐ malaria

(b)

**sickle-cell
allele in Africa**

☐ 1– 5 %
☐ 5 –10 %
☐ 10 – 20 %
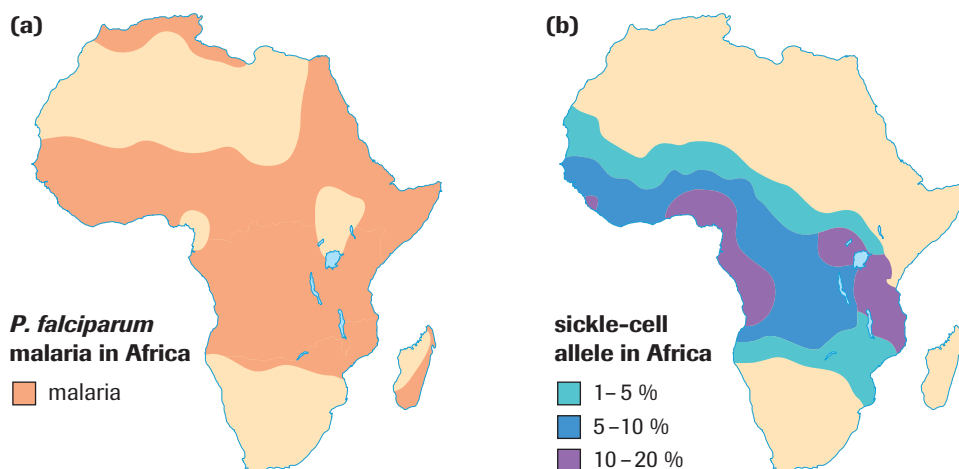
Figure 5
Of the 120 million new cases of malaria each year, about 1 million are fatal. The prevalence of malaria in Africa in **(a)** closely matches the distribution of the sickle-cell allele in **(b)**. The percentages are estimates of a distribution range.

The sickle-cell allele is only common where it provides an overall advantage to the individual. In populations where it has an overall harmful effect, it does not persist. This pattern demonstrates an important relationship between mutations and gene pool changes in a population:

- Harmful mutations occur frequently, but they are selected against and, therefore, these mutant alleles remain extremely rare.
- Beneficial mutations are rare, but they are selected for and, therefore, these mutant alleles may accumulate over time.

Case Study

Antibiotic-Resistant Bacteria

An article in the *Canadian Medical Association Journal* (July 2001) reported an alarming six-fold increase in the rate of antibiotic resistance in Canada between 1995 and 1999. In addition to added health risks, fighting antibiotic resistance can be expensive. Across Canada, the cost is estimated at $50 to $60 million a year.

In 1996, doctors took samples of bacteria from a patient suffering from tuberculosis, a lung infection caused by the bacterium *Mycobacterium tuberculosis.* Cultures of the bacteria found it to be sensitive to a variety of antibiotics, including rifampin. The patient was treated with rifampin and initially responded so well that the lung infection seemed to be over. Soon after, however, the patient had a relapse and died. An autopsy revealed that bacteria had invaded the lungs again in large numbers. Cultures of these bacteria were found to be sensitive to many antibiotics, but resistant to rifampin. DNA sequencing revealed that a certain bacteria's gene had a single base-pair mutation that was known to confer resistance to rifampin. Doctors compared the new bacteria culture with the original culture and found that the sequences were identical except for this single mutation. Researchers then examined more than 100 strains of bacteria from other tuberculosis patients living in the same city at the same time. None of these

bacteria had the same genetic code as the rifampin-resistant bacteria obtained in the autopsy. When doctors had begun administering rifampin, the bacteria in the patient had been subjected to a new environmental selective agent, one that gave the mutant strain a major adaptive advantage.

The pattern in this story is not uncommon, but evolution offers some hope as well as alarm. Many traits that provide antibiotic resistance are harmful to the bacteria. For example, a strain of *E. coli* bacteria possesses a plasmid with a gene that enables it to produce an enzyme called b-lactamase. This enzyme gives the bacterium resistance to the antibiotic ampicillin. However, there is a cost for this resistance: to maintain its antibiotic resistance, the bacterium must devote cellular resources to producing the enzyme and to making copies of the plasmid before cell division, slowing its growth rate. In another example, the bacterium *Mycobacterium tuberculosis* normally produces catalase, a beneficial but non-essential enzyme. This enzyme, however, activates the antibiotic isoniazid, which destroys the bacterium. Bacteria that have a defective catalase gene are, therefore, resistant to isoniazid—as it cannot be activated in the absence of catalase—but they lack the benefits normally provided by the enzyme. As a result of these costs of resistance, when an antibiotic is not present, natural selection often favours those bacteria that do not carry antibiotic-resistant alleles.

Non-Random Mating

Individuals that mate and reproduce frequently make a substantial contribution to the gene pool of later generations. **Sexual selection** favours the selection of any trait that influences the mating success of the individual. The traits favoured in sexual selection include **sexual dimorphism** (i.e., striking differences in the physical appearance of males and females) and behavioural differences between the sexes. The most common forms of sexual selection result from female mate choice and from male-versus-male competition. In some species, females choose mates based on physical traits, such as bright coloration, or behavioural traits, such as courtship displays and song. In other species, males are equipped with physical features that assist them in establishing control of and defending their territory against other males (**Figure 6**). This territory provides an area to which they can attract, and sometimes forcibly detain, the females with which they mate. Such traits are not produced by selective pressures from environmental conditions; if they were, both sexes would be expected to possess them.

Many species have evolved features that are a compromise between different selective pressures. Sexual selection has produced traits that are beneficial for mating, but may otherwise be detrimental. Avoiding predators is not made easier, for instance, by brilliant plumage or a distinctive song.

sexual selection differential reproductive success that results from variation in the ability to obtain mates; results in sexual dimorphism and mating and courtship behaviours

sexual dimorphism striking differences in the physical appearance of males and females not usually applied to behavioural differences between sexes

+ EXTENSION 🔊

The Hardy-Weinberg Principle "Agents of Change"
This Audio Clip summarizes the "agents of change" predicted by the Hardy-Weinberg Principle and explains how each can change allele frequency and genotype frequency of a population.

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Figure 6
Sexual dimorphism may take the form of a physical feature. For example, female fiddler crabs lack the special enlarged right claw of the male as seen here.

Sexual diversity is not limited to animal populations. Most plants do not select mates, but they do need to attract or use various agents—such as insects, birds, and bats—to assist in pollination. Flowers and scents are the most obvious sexual features that have evolved through natural selection.

Not all species show obvious sexual dimorphism. In some species of penguin, males and females look so similar that even they have a hard time telling each other apart (**Figure 7**). A male picks up a stone and drops it at the feet of a would-be mate. If the other penguin happens to be a male, the gift is firmly rejected.

Figure 7
Penguin species that lack sexual dimorphism instead have behaviours that allow them to distinguish males from females.

W W W *WEB Activity*

Web Quest—Hardy–Weinberg and the Colour of Guppies

The use of computer models is very important in a lot of current scientific research. Many multi-disciplinary teams work together on common projects, and the use of models often allows these teams to share findings. In this Web Quest, you and the members of your class will form a research team exploring variation in coloration of a population of guppies. In groups, you will explore several computer models of the Hardy–Weinberg principle. Each group will then use one of these models to explain the colour variations, and then present the results to the rest of the research group. The entire multi-disciplinary research team will then reach a consensus explanation.

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INVESTIGATION 21.1 *Introduction*

Agents of Change

Population size, genetic drift, and natural selection all affect allele frequencies. Using coloured beads to model alleles in a population, you will design and conduct an investigation to explore how population size, genetic drift, and natural selection effect changes in allele frequency. How can the influence of these factors be predicted?

Report Checklist

○ Purpose	● Design	● Analysis
● Problem	○ Materials	● Evaluation
● Hypothesis	● Procedure	● Synthesis
○ Prediction	● Evidence	

SUMMARY   *Changes in Gene Pools*

- When Hardy–Weinberg conditions are not met, the gene pool of a population may change over time.

- In small populations, genetic drift (including the bottleneck and founder effects) and gene flow may change allele frequencies and genetic diversity.

- Migration may cause gene flow, in which alleles are removed from the gene pool of one population and added to another.

- Mutation may change the frequency of existing alleles and add new alleles to the gene pool.

- Natural selection may change allele frequencies in a gene pool by selecting against harmful alleles and selecting for beneficial alleles

- Non-random mating may cause some alleles to occur more or less frequently in the gene pool of the next generation.

1. Define genetic drift and genetic flow, offering two examples to illustrate each definition.

2. Suggest three types of organisms that might produce founder populations. Explain the process that results in this effect.

3. The world's population of cheetahs is almost identical genetically. Male cheetahs are known to have low sperm counts and the species in general has a low resistance to many infectious diseases. All cheetahs are thought to be homozygous at over 99.9 % of their gene loci. Explain how a severe genetic bottleneck effect in the past could account for these observations.

4. If variation in species were solely a result of genetic recombination during sexual reproduction, how would that limit the evolution of species?

5. Relate two ways in which alleles can become fixed in a population.

6. It is thought that a billion prairie dogs once populated an area of more than 100 million ha. Their current territory has been reduced and fragmented to less than 1 % of this original space. Predict the impact of these changes in habitat on the prairie dog gene pool, as well as on the survival of the species.

7. The present population of whooping cranes suffers from low genetic diversity and susceptibility to a variety of diseases. Which of the founder effect, the bottleneck effect, and gene flow are likely to account for these observations?

8. Many insect species have evolved resistance very rapidly to a range of pesticides. Like other species, insects exhibit variation in physical, chemical, and behavioural traits.
   (a) Describe how an insect species would evolve resistance to a pesticide newly introduced into its environment.
   (b) How might high rates of reproduction and the short duration of insect generations affect their evolution?
   (c) How might an understanding of the evolution of pesticide resistance influence how you use pesticides or alternative methods of insect control?

9. In recent years, many Africans who are carriers of the allele for sickle-cell anemia have emigrated from malaria-stricken areas in Africa to North America. Has this influenced the biological role of the sickle-cell allele? Explain.

10. Suggest how large antlers or bright coloration could be a disadvantage for males of some species.

11. Although, in theory, an individual could mate at random with other members of a large population, this seldom occurs. Under most natural conditions, individuals tend to mate with nearby members of the same species, especially if they are not very mobile. Alternatively, individuals choose mates that share similar traits; for example, toads (and often humans) tend to pair according to size.
    (a) How might inbreeding (the mating of closely related individuals) lead to an increase in the number of sometimes harmful recessive phenotypes? Relate your answer to either a population of cheetahs in the wild or a population of golden retrievers in a breeding kennel.
    (b) Does nonrandom mating result in changes to population phenotype frequencies, genotype frequencies, or allele frequencies?

12. In many zoos, artificial insemination of female tigers is becoming common practice. Semen is collected from male tigers in various zoos around the world, frozen in liquid nitrogen, and shipped to zoos where it is used to inseminate female tigers in estrus.
    (a) Why do you think this is being done?
    (b) How might this affect the gene pool of tiger populations?
    (c) Do you think these efforts are enough to prevent a genetic bottleneck from occurring? Explain.
    (d) What conditions do you think are necessary to ensure the genetic diversity of zoo populations?

13. Insect resistance to pesticides is estimated to cost tens of millions of dollars per year in Canada. The Colorado potato beetle, for example, developed resistance to five different pesticides over a period of only 15 years. Predict how such evolutionary consequences might affect and concern consumers, ecologists, pesticide companies, organic farmers, and plant breeders.

INVESTIGATION 21.1

Agents of Change

In this investigation, you will design and conduct experiments to examine the influence of population size, genetic drift, and natural selection on the rate of evolution, by measuring changes in allele frequencies.

Work with your partner to develop a design and conduct experiments for Parts 1, 2, and 3, using or modifying the procedure below. Prepare data collection tables. Submit your modified experimental design to your teacher for approval before conducting each of your three experiments.

Problem

How do genetic drift and natural selection influence the allele frequency within a population?

Materials

80 or more beads in colour A (to represent allele *R*)
80 or more beads in colour B (to represent allele *r*)
large opaque container (to represent a gene pool)

✋ **Immediately pick up any beads that drop on the floor, as they might cause someone to slip.**

Procedure

1. Place 40 beads of each colour (80 beads in total) in the large opaque container.
2. Thoroughly mix the "alleles" (beads) in the "gene pool" (container).
3. At random, reach into the gene pool and take out 20 pairs of alleles to represent offspring genotypes that contribute to the next generation.
4. Determine and record the number of each genotype (e.g., 5 *RR*, 7 *Rr*, 8 *rr*).
5. Record the F_1 allele frequencies as decimal values. For example, divide 17 *R* and 23 *r* by 40 to get the frequencies of 0.425 *R* and 0.575 *r*, respectively.
6. Place the next generation of 80 beads in the "gene pool" container in the same proportions of allele frequencies as the "offspring" (e.g., 0.425 × 80 = 34 *R*, 0.575 × 80 = 46 *r*).
7. Repeat steps 3 to 6 for four additional generations.

Report Checklist

○ Purpose	● Design	● Analysis
● Problem	○ Materials	● Evaluation
● Hypothesis	● Procedure	● Synthesis
○ Prediction	● Evidence	

Part 1: Random Mating, No Selection

8. Run at least two trials in which you use large populations and meet the conditions of the Hardy–Weinberg Principle. These trials act as your control in Part 2 and Part 3.

Part 2: Genetic Drift

9. Run at least two trials in which you examine the influence of population size on the degree and rate of genetic drift. Choose two or more starting populations of different sizes. As an option, you may also wish to model a founder effect.

Part 3: Natural Selection

10. Run at least two trials in which natural selection occurs. You might model a favoured homozygous genotype in which, for example, *RR* offspring might be twice as successful as other genotypes. If so, you would need to allow for the increased ratio of offspring contributing to the next generation, while maintaining a stable, large population. As an option, you could investigate selection against a homozygous lethal allele by assuming that each time a specific homozygous allele pair is selected, it dies, and you have to keep adding pairs until you have 20 offspring. Another option is to investigate a selective advantage for a dominant phenotype.

Analysis and Evaluation

(a) Make a separate graph of the data you collected for each of Parts 1, 2, and 3, by plotting allele frequency versus generation. On each graph, use two different colours on the same set of axes to represent the *R* and *r* alleles.

(b) How did population size influence the degree and rate of evolutionary change? Did any alleles become fixed in a population? In what size populations might you expect it to be relatively common for alleles to become fixed? Why?

(c) What conditions occur in nature that result in small populations?

(d) How did natural selection influence the degree and rate of evolutionary change? Did any alleles become fixed in the population?

(e) Were your results unusual compared with similar conditions in other groups?

(f) For each of your experiments in which evolution did occur, which of the five conditions of the Hardy–Weinberg Principle was not met?

Synthesis

(g) Assume you introduced a single new mutant allele to your population. Explain what you expect would happen under each of the following conditions:

(i) The mutant is harmful and the population size is large.

(ii) The mutant is harmful and the population size is small.

(iii) The mutant is beneficial and the population size is large.

(iv) The mutant is beneficial and the population size is small.

(v) A beneficial mutant is introduced and the population is observed four generations later.

(vi) A beneficial mutant is introduced and the population is observed 400 generations later.

Outcomes

Knowledge

- describe the Hardy–Weinberg Principle and explain its importance to population gene-pool stability and the significance of non-equilibrium values (21.1)
- describe the factors that cause the gene pool diversity to change, i.e., genetic drift, gene flow, non-random mating, bottleneck effect, migration, mutation, natural selection, and founder effect (21.2)
- apply quantitatively the Hardy–Weinberg Principle to observed and published data to determine allele and genotype frequencies (21.1)
- describe the molecular basis of gene-pool change and the significance of these changes over time, i.e., mutations and natural selection (21.2)

STS

- explain that science and technology have both intended and unintended consequences for humans and the environment (21.2)
- explain how concepts, models, and theories are often used in interpreting and explaining phenomena (21.1)

Skills

- ask questions and plan investigations (21.2)
- conduct investigations and gather and record data and information by: designing and performing an investigation to demonstrate population growth and gene-pool change (21.2)
- analyze data and apply mathematical and conceptual models by: calculating and interpreting problem-solving exercises involving the Hardy–Weinberg Principle (21.2)
- work as members of a team and apply the skills and conventions of science (all)

Key Terms 🔊

21.1

allele frequency

fixed frequency

21.2

genetic drift

gene flow

founder effect

sexual selection

bottleneck effect

sexual dimorphism

Key Equation

Hardy–Weinberg Equation

If p = frequency of allele A and q = frequency of allele a, then

$$p + q = 1$$
$$(p + q)^2 = 1^2$$
$$p^2 + 2pq + q^2 = 1$$

where p^2 = frequency of genotype AA, $2pq$ = frequency of genotype Aa, and q^2 = frequency of genotype aa

▶ MAKE a summary

1. Evolution in its simplest form is the change in the gene pool of a species over time. According to the Hardy–Weinberg Principle, gene pool changes do not occur in populations if certain conditions are met. Write a detailed article to address this apparent contradiction. Explain how each of the following may cause gene pool change:
   - random chance
   - gene flow
   - small population size
   - natural selection
   - mutation
   - sexual selection

2. Revisit your answers to the Starting Points questions at the start of the chapter. Would you answer the questions differently now? Why?

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The following components are available on the Nelson Web site. Follow the links for *Nelson Biology Alberta 20–30*.

- an interactive Self Quiz for Chapter 21
- additional Diploma Exam-style Review Questions
- Illustrated Glossary
- additional IB-related material

There is more information on the Web site wherever you see the Go icon in the chapter.

✚ EXTENSION 🔊

CBC 📻 radio**ONE** QUIRKS & QUARKS

Fowl Play: Disappearing Diversity

Dr. Mary Delany (assistant professor at the University of California, Davis), Dr. Donald Shaver (former head of the Shaver group, one of Canada's largest poultry breeders), Dr. Frank Robinson (professor of poultry management and physiology at the University of Alberta), and Dr. David Notter (Virginia Tech) discuss their various viewpoints on the genetic issues of Canada's commercial poultry. The gene pool for these birds is very small, and outside stock to maintain the gene pool is disappearing.

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Many of these questions are in the style of the Diploma Exam. You will find guidance for writing Diploma Exams in Appendix A5. Science Directing Words used in Diploma Exams are in bold type. Exam study tips and test-taking suggestions are on the Nelson Web site.

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DO NOT WRITE IN THIS TEXTBOOK.

Part 1

1. Identify which of the following conditions is not necessary to maintain Hardy-Weinberg equilibrium in a population.
   A. Mating must be random.
   B. The population must be large.
   C. Initial allele frequencies must be equal.
   D. Immigration or emigration cannot occur.

2. A small number of individuals establish a new population with a distinct set of allele frequencies that is isolated from the parent population. This is referred to as
   A. evolution
   B. a bottleneck
   C. genetic drift
   D. the founder effect

3. When a population does not meet the conditions necessary for maintaining Hardy–Weinberg equilibrium, it will
   A. evolve
   B. increase rapidly in population size
   C. result in all allele frequencies becoming equal
   D. usually decline in numbers, leading to extinction

4. Four percent of an African population is born with a severe form of sickle-cell anemia (*ss*). The percentage of the population that will be heterozygous (*Ss*) for the sickle-cell gene is
   A. 4 %
   B. 16 %
   C. 32 %
   D. 96 %

5. The bottleneck effect is *not* associated with
   A. increases in mutation rate
   B. small populations
   C. increases in the risk of extinction
   D. enhancement of the influence of genetic drift

6. Which of the following traits is probably *not* associated with sexual selection?
   A. defending a nesting territory
   B. extreme running speed in pronghorn antelope
   C. the large, bright tail feathers of a male peacock
   D. differences in size between male and female wood buffalo adults

7. Antibiotic resistance is largely a result of
   A. genetic drift
   B. many random mutations
   C. an evolutionary response to a change in the environment
   D. the same individual bacterium being repeatedly exposed to antibiotics

8. A gene for which there exists only a single allele in the population are referred to as
   A. fixed
   B. recessive
   C. dominant
   D. homozygous

9. For each of the factors given below, determine the number that would be expected to increase the rate of genetic change over time. (Record all four digits of your answer in lowest-to-highest numerical order.)
   NR
   1. large population
   2. random breeding
   3. migration
   4. stable environment
   5. non-random breeding
   6. changing environment
   7. small population
   8. no migration

Part 2

10. **Outline** in a list the conditions that must be met to satisfy the Hardy–Weinberg equilibrium in a population. Clearly **explain** how the failure to meet any one of the conditions can lead to evolutionary change.

11. If beneficial mutations are much more rare than harmful ones, **how** can they have such an important role in evolution?

12. **Illustrate**, with an example, how random chance can have a greater effect on small populations than on larger populations.

13. Sketch **Figure 1** into your notebook, adding relevant labels. **Identify** and **describe** the effect that your sketch illustrates.
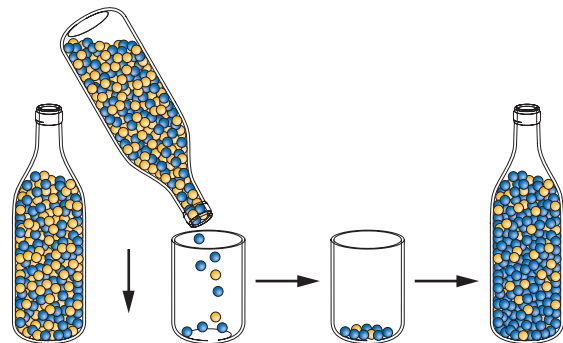
Figure 1

14. **Outline** in a list and **explain** some of the factors that have led to the rapid evolution of antibiotic resistance among many bacteria.

15. Would you expect bacteria occurring in wildlife, or in domesticated animals, to show signs of antibiotic resistance? **Explain** your answer.

16. A small population of pygmy mammoths measuring only
DE 2 m in height once lived on a small island off the coast of California. Biologists believe this is an example of a population that descended from a few large mammoths that reached the island more than 50 000 years ago. In a unified response, **explain** how the following factors might have contributed to the formation of this unusual species:
    • the small founding population,
    • the remote location, and
    • natural selection on this island.

17. Before the large-scale movement of people around the world, including the slave trade, the sickle-cell allele was extremely rare except in regions where malaria occurs. Based on this distribution, is it accurate to describe the allele as harmful? **Explain**.

18. In a population of 40 000 bats, you have identified two distinct phenotypes that result from two alleles at a single gene locus. One allele (C) produces dark brown hair and the other (c) produces cinnamon-coloured hair. If only 16 bats are cinnamon-coloured, **determine** the allele frequencies in the population. Assume the population is in Hardy–Weinberg equilibrium.

19. Suppose that 1 in 400 people in a large population have a recessive disorder. Apply the Hardy–Weinberg Principle to **determine** the proportion of individuals who are carriers of (i.e., heterozygous for) this disorder.

20. **Predict** how the genetic diversity of a population of lake trout from a small lake in northern Alberta would compare with the genetic diversity of a population of lake trout in Lake Winnipeg. **How** might you investigate your prediction?

21. In order to mate, sage grouse males gather in "leks" and engage in unusual display behaviours in hopes of attracting females. **How** would this behaviour influence the Hardy–Weinberg equilibrium in such a population?

Use the following information to answer questions 22 to 24.

An unusual group of black bears live in the rainforests of British Columbia. The Kermode (spirit) bears are white, a trait coded for by a recessive allele (k). The more common black colour is coded for by a dominant allele (K). On Princess Royal Island, approximately 10 % of the bears are white in colour.

22. **Determine** the frequencies of both the recessive and
DE dominant alleles in the population.

23. **Determine** the percentage of the population you would
DE expect to be carriers of the K allele.

24. Assume that the bear population behaves according to the
DE Hardy–Weinberg equation. **Predict** what would happen to the frequencies of K and k, if the entire population doubled in size.

Use the following information to answer questions 25 to 27.

The wood buffalo population in Elk Island National Park began with the introduction of a small founder population of 11 animals whose parents lived in Wood Buffalo National Park. Recent DNA studies indicate that the genetic diversity of the Elk Island population is much lower than that of the Wood Buffalo National Park population.

25. **Explain** the lower genetic diversity in the Elk Island
DE population.

26. **Identify** the population that would be most able to
DE respond to environmental changes? **Justify** your choice.

27. A wildlife officer wants to establish a population of wood
DE buffalo elsewhere, using animals from the Elk Island captive population. **Describe** what precautions might the officer take to increase the chances of success?

28. The majority of the Afrikaner population in South Africa is descended from a single shipload of Dutch immigrants in 1652. Compared to the Dutch population, these descendants have a much higher incidence of such rare genes as the ones that cause Huntington's disease and the enzyme defect *variegate porphyria*. **Describe** the most likely explanation for these observations.